

Exhibit A

**Human
Molecular Genetics**

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Author: Keyword(s):

Go [] []

Year: [] Vol: [] Page: []

OXJ
Journ:

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Contents: Volume 8, Number 12 November 1, 1999 [Index by Author]

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[] CORRIGENDUM

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Clear [] Get All Checked Abstract(s)

ARTICLES: []Cover sheet
for Nov. 1999
issue
my

☐ I Miguel-Aliaga, E Culetto, DS Walker, HA Baylis, DB Sattelle, and KE Davies
The Caenorhabditis elegans orthologue of the human gene responsible for spinal
muscular atrophy is a maternal product critical for germline maturation and
embryonic viability
Hum. Mol. Genet. 1999 8: 2133-2143; doi:10.1093/hmg/8.12.2133
[Abstract] [Full Text]

☐ AG Bijvoet, H Van Hirtum, MA Kroos, EH Van de Kamp, O Schoneveld, P Visser, JP
Brakenhoff, M Weggeman, EJ van Corven, AT Van der Ploeg, and AJ Reuser
Human acid alpha-glucosidase from rabbit milk has therapeutic effect in mice with
glycogen storage disease type II
Hum. Mol. Genet. 1999 8: 2145-2153; doi:10.1093/hmg/8.12.2145
[Abstract] [Full Text]

☐ AD Simmons, MM Musy, CS Lopes, LY Hwang, YP Yang, and M Lovett
A direct interaction between EXT proteins and glycosyltransferases is defective in
hereditary multiple exostoses
Hum. Mol. Genet. 1999 8: 2155-2164; doi:10.1093/hmg/8.12.2155
[Abstract] [Full Text]

☐ A Oka, G Tamiya, M Tomizawa, M Ota, Y Katsuyama, S Makino, T Shiina, M Yoshitome,
M Iizuka, Y Sasao, K Iwashita, Y Kawakubo, J Sugai, A Ozawa, M Ohkido, M Kimura, S
Bahram, and H Inoko

TITLE Association analysis using refined microsatellite markers localized a susceptibility locus for peristasis vulgaris within a 111 kb segment telomeric to the HLA-C gene
JOURNAL Hum. Mol. Genet. 8 (12), 2165-2170 (1999)
PUBLISHED 10545595
REFERENCE 2 (bases 1 to 1143)
AUTHORS Taniya, G., Tomiawa, M., Makino, S., Oka, A., Nakajima, K., Kimura, M. and Inoko, H.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1999) Akira Oka, Tokai University School of Medicine, Division of Molecular Life Science; Bohbedai, Isenhera, Kanagawa 259-1193, Japan (E-mail: oka246@is.tcu-u-tokai.ac.jp, Tel: 81-463-93-1121 (ex. 2579), Fax: 81-463-94-8884)
FEATURES Location/Qualifiers
Source 1. 1143
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CDS /mol_type="mRNA"
ORIGIN /db_xref="taxon:9606"
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Best local similarity /map="6p21.3"
Matches 886; Conservative /sex="male"
99.14; Score 883; DB 9; Length 1143; /cell_type="epidermal keratinocytes"
99.44; Pred. No. 1.7e-190; Mismatches 5; Indels 0; Gaps 0; 1. 1143
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316.726

1143 bp mRNA linear PRI 08-DEC-1995
complete cds.

REFERENCE	AUTHORS
1 (stiles)	Ota, A., Tamiya, G., Tomizawa, M., Ota, M., Katsuyama, Y., Makino, S., Shima, T., Yoshitome, M., Iizuka, M., Saseo, Y., Iwashta, K., Kawakubo, Y., Sugai, J., Ozawa, A., Ohkido, M., Kimura, M., Bahram, S. and Inoko, H.

TITLE Association analysis using refined microsatellite markers localized a susceptibility locus for periodontitis vulgaris within a 111 kb segment telomeric to the HLA-C gene
JOURNAL Hum. Mol. Genet. 8 (12), 2165-2170 (1999) **X**
PUBLISHED 10545595
REFERENCE 2 (bases 1 to 1143)
AUTHORS Tamaiya, G., Tomiawa, M., Makino, S., Oka, A., Nakajima, K., Kimura, M. and Inoko, H.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1999) Akira Oka, Tokai University School of Medicine, Division of Molecular Life Science; Bobbedai, Isenhera, Kanagawa 259-1193, Japan (E-mail: toka24@is.icc.u-tokai.ac.jp, Tel: 81-463-93-1121 (ex. 2579), Fax: 81-463-94-8884)
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253 CTTCTGGGGTCCCGAGCACCAAGACTCAGACCACCCAGCTTTGGGGCCAGTACATA 312
Qy 61 GCCATGATCTCAACTGGAAGCTCTGGGGATCTTGCTTTGCTGCACACCAAGGC 120
313 GCCATGATCTCAACTGGAAGCTCTGGGGATCTTGCTTTGCTGCACACCAAGGC 372
Qy 121 ATCTCAGGGCGCAGAGGCCACCCCTCTCAACCCACCCGACAGACCGAGAGAGGCGC 180
373 ATCTCAGGGCGCAGAGGCCACCCCTCTCAACCCACCCGACAGACCGAGAGAGGCGC 432
Qy 181 TCCCAACATTGCTCAGAGGCCCCCGACGATCCCGGTGAACCTTGGCCAGGGGACCCCT 240
433 TCCCAACATTGCTCAGAGGCCCCCGACGATCCCGGTGAACCTTGGCCAGGGGACCCCT 492
Qy 241 CTCTTTGAAGATCTTCGCTACCGCCCGCCAGTCTCTCTGAGAGACCTTGCTGAAC 300
493 CTCTTTGAAGATCTTCGCTACCGCCCGCCAGTCTCTCTGAGAGACCTTGCTGAAC 552
Qy 301 GAGGTCTGGCCCCCTGAACCGCTTAAGAGGATCTTCTCAACTCCCGGGCTGACGAC 360
553 GAGGTCTGGCCCCCTGAACCGCTTAAGAGGATCTTCTCAACTCCCGGGCTGACGAC 612
Db 361 CTTGGCCGGCAGAGCCCGACGCCCCAGAAACCCCTGGGCTCTCGCCCTGAGGTGAC 420
613 CTTGGCCGGCAGAGCCCGACGCCCCAGAAACCCCTGGGCTCTCGCCCTGAGGTGAC 672
Qy 421 AACCGACTCAGAGAGGCGACGACTGACCCACCCCGGAGAGTACAGATTAAGAGT 480
673 AACCGACTCAGAGAGGCGACGACTGACCCACCCCGGAGAGTACAGATTAAGAGT 732
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Qy	115	AGAGGCACTTCAGGCGAGGAGGCGACCCCTCTCA	CCACCCGAGAGGACCGAGAGAG	174	
Db	27085	ACAGGCACTCTCAGGCGAGGAGGCGACCCCTCTCA	CCACCCGAGAGGACCGAGAGAG	27144	
Qy	175	GCAGGCTCCCCAAATTGCTCAGGCGCCCAATCCCCG	GTGACCTTGGCCAGGGGCA	234	

Db	27145	GAGAGCTCCCAACATGTCTCAGGACCCCCAGTCCCGGTGACCTTGCCAGGAGCA	27204
Qy	235	CCCCCTCTTTTGAAGATCTCCGCTTACCCGCCCCAGTCTGTCTCTGAGAGACTCTGCT	294
Db	27205	CCCCCTCTTTTAAAGATCTCCGCTTACCCGCCCCAGTCTGTCTCTGAGAGACTCTGCT	27264
Qy	295	GAAACTGAGTCTGAGCCCCCTGAAACCGCTGAGACGATCTCTCAACTCTCCGAGCT	354
Db	27265	GAAACTGAGTCTGAGCCCCCTGAAACCGCTGAGACGATCTCTCTCAACTCTCCGAGCT	27324
Qy	355	GACGACCTTGTGCCCCGAGAGACCCAGCCCCAGAAAACCCCTGTGCTCTGCCCCTGAG	414
Db	27325	GACGACCTTGTGCCCCGAGAGACCCAGCCCCAGAAAACCCCTGTGCTCTGCCCCTGAG	27384
Qy	415	GTGGACAAACGACCTGAGAGAGAGGACGACCTGAGACCCACCCCGGGAAGATGACATTA	474
Db	27385	GTGGACAAACGACCTGAGAGAGAGGACGACCTGAGACCCACCCCGGGAAGATGACATTA	27444
Qy	475	TGAGATCCCTCAGCCGTTCTGTCTCCAGGACATCTCCAGGACCCACGCCCTCTCCACCC	534
Db	27445	TGAGATCCCTCAGCCGTTCTGTCTCCAGGACATCTCCAGGACCCACGCCCTCTCCACCC	27504
Qy	535	TCTGATTCCTCCCGGAATTCTTCCCAATTAGCTATCTCTTAACTCTTCTCAATTCC	594
Db	27505	TCTGATTCCTCCCGGAATTCTTCCCAATTAGCTATCTCTTAAACTCTTCTCTCAATTCC	27564
Qy	595	CTGGATTATTTTGAACCCGTAAGGTGTTCTCAATATTTCTGTCCCCCTCGAGA	654
Db	27565	CTGGATTATTTTGAACCCGTAAGGTGTTCTCAATATTTCTGTCCCCCTCGAGA	27624
Qy	655	TCCATTAATTAGTCTCAATCCGCCGTTTTTCTCTGACAGCTTAAGCTTACTCTCTTA	714
Db	27625	TCCATTAATTAGTCTCAATCCGCCGTTTTTCTCTGACAGCTTAAGCTTACTCTCTTA	27684
Qy	715	CCTGCGCTCCAGGCTCCGCCCCCACTTACCTCCACCCGAGTCTCTGCGCGGCGAGATG	774
Db	27685	CCTGCGCTCCAGGCTCCGCCCCCACTTACCTCCACCCGAGTCTCTGCGCGGCGAGATG	27744
Qy	775	CTGGGCAAGGCTATAGTATCTGTTCCTTCTGCACTGTGTGCGCGGCGAGAACT	834
Db	27745	CTGGGCAAGGCTATAGTATCTGTTCCTTCTGCACTGTGTGCGCGGCGAGAACT	27804
Qy	835	ATCAGTAGACAGCTGTGCTCCATGAAACGAAAAATTAATAATGTTTTCTTAA	891
Db	27805	ATCAGTAGACAGCTGTGCTCCATGAAACGAAAAATTAATAATGTTTTCTTAA	27861

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	9	
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LOCUS		
DEFINITION	Sequence 4 from Patent WO02064831.	55050 bp DNA linear PAT 24-OCT-2002
ACCESSION	AX522117	
VERSION	AX522117.1	GI:24411002
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens Eukaryote; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	1	
AUTHORS	Lench,N.J., Allen,M.J. and Nicholls,R.K.	
TITLE	Test and model for inflammatory disease	
JOURNAL	Patent: WO 02064831-A 4-22-AUG-2002;	
FEATURES	Oxagen Limited (GB) Location/Qualifiers	
Source	/organism="Homo sapiens" /mol_type="unassigned DNA"	
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Query Match	87.0%; Score 775; DB 6;	Length: 55050;
Best Local Similarity	99.7% ; Pred. No. 4.9e+16;	
Matches 775; Conservative	1; Mismatches	0; Gaps 0;
	Ideals	

EXhibit C

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Alignment Scores:
Pred. No.: 2.08e-24 Length: 891
Score: 808.00 Matches: 136
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-994-365-2 (1-136) x AK477387 (1-891)

Qy 1 MettLeuAentTpybLeuLeuGlytyleuValleuCybLeuHietHrArglytyle 20
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Qy 21 SerGlySerGlyGlytyleuSerHietHrArglytyleuValleuValleuSer 40
Db 124 TCAAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 183
Qy 41 ProThrLeuProGlnGlyProProValProGlyAspProTyrProGlyValAspProLeu 60
Db 184 CCAACATGCTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
Qy 61 PheGluAspProProGlnGlyProProValProGlyAspProTyrProGlyValAspPro 80
Db 244 TTTGAAAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 303
Qy 81 ValTyrProProGlnGlyProProValProGlyAspProTyrProGlyValAspPro 100
Db 304 GTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 363
Qy 101 TrpProAlaGlyProGlnGlyProProValProGlyAspProTyrProGlyValAspPro 120
Db 364 TGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 423
Qy 121 ArgProGlnGlyGlyProProValProGlyAspProTyrProGlyValAspPro 136
Db 424 CGACCTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 471

RESULT 2
LOCUS CQ722444 1143 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 8378 from Patient MO02068579.
ACCESSION CQ722444
VERSION CQ722444.1 GI:42283301
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kites, such as nucleic acid arrays, comprising a majority of
humans or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent, WO 02068579-A 8378 06-SEP-2002;
FEATURES
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1. 1143
Location/Qualifiers
/organism="Homo sapiens"
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Alignment Scores:
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Score: 808.00 Matches: 136
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-994-365-2 (1-136) x CQ722444 (1-1143)

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Qy 21 SerGlySerGlyGlytyleuSerHietHrArglytyleuValleuValleuSer 40
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Db 496 TTTGAAAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 555
Qy 81 ValTyrProProGlnGlyProProValProGlyAspProTyrProGlyValAspPro 100
Db 556 GTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 615
Qy 101 TrpProAlaGlyProGlnGlyProProValProGlyAspProTyrProGlyValAspPro 120
Db 616 TGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 675
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ACCESSION AB031480
VERSION AB031480.1 GI:5339433
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (sites)
Oka, A., Tamaya, G., Tomizawa, M., Oka, M., Katsuyama, Y., Makino, S.,
Shino, T., Yoshitome, M., Litzke, M., Saeo, Y., Iwashita, K.,
Kawakubo, Y., Sugai, J., Ozawa, A., Ohkido, M., Kimura, M., Bahram, S.
and Inoko, H.
Association analysis using refined microsatellite markers localizes
a susceptibility locus for psoriasis vulgaris within a 111 kb
segment telomeric to the HLA-C gene
Hum. Mol. Genet. 8 (12), 2165-2170 (1999)
JOURNAL Submitted (25-AUG-1999) Akira Oka, Tokai University School of
Medicine, Division of Molecular Life Science, Bohseidai, Isehara,
Kanagawa 259-1193, Japan (E-mail:oka24@is.jcc.u-tokai.ac.jp,
Tel:81-463-93-1121 (ex.2579), Fax:81-463-94-8884)
FEATURES
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1. 1143
Location/Qualifiers
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Pred. No.: 2.49e-24 Length: 1143
Score: 808.00 Matches: 136
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY	39	GLYSERPROTHLEUPROGINGLYPROPROVALPROGLYASPROTPROGLYALAPRO	58
Db	27148	GGCTCCCCAATGGCTCAGAGGGCCCCCAAGTCCCGCGTACCTTGGCCAAGGGGACCC	27207
QY	59	PROLEUPHEGIUASBPBROPROTHNARGPROSERARGPROTPARGAPLEAPROGLIN	78
Db	27208	CCTCTCTTGAAGAGCTCTCGCCTCAACCGCCCCCAAGTGCTCCCTGAAAGACCTGCTCGAA	27267

QY	19	GlyLeSerGlySerGluGluGlyAspSerHisLeuProAlaGluAspArgGluGluAla	38
Db	27099	GGCATCTCAGGACGAGGGCCACCCTCTCAACCCACCGGAGAGGACCGAGAGGAGCA	27158
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QY	59	ProIleuHegIuAspProProProThrArgProSerArgProTyrAlaArgAspLeuProGlu	78
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QY	79	ThrGlyValTyrProProGluProProAlaGlyThrAspProProGlnProProAlaPro	98
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RESULT 13
AL662867/c
LOCUS

AL662867 70288 bp DNA linear PRI 24-APR-2002

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Qy	81 AIAEGLYPProGInPProGluPAspPThrPProPProAlaPProGluValaLAspAsnArgPro	100
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Qy	101 GInGluGluPProAspLeuAspPProPProArgGluGluTyrArg	114
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DEFINITION	Homo sapiens clone	UWGC:y2c027	from 6p21,	complete sequence.
ACCESSION	AC004195			
VERSION	AC004195.1	GI:3980474		
KEYWORDS	HTG.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK

1 (bases 1 to 40878)
Jameh, M., Guillaudeau, T., Vu, Q., Kutyavin, T., Harter, H. and
Gerashchik, D. B.
Large scale sequence analysis of the human MHC class I region
unpublished (1998)
Fred Hutchinson Cancer Research Center

2 (bases 1 to 4087).
Geraghty, D.E. and Olson, M.V.
Direct Submission
Submitted (23-FEB-1998) Human Genome
Database, Los Angeles, CA, USA
Accession No. AF000001

REFERENCE
AUTHORS
TITLE
JOURNAL

Washington, Box 351145, University of
3 (bases 1 to 40878), Seattle, WA 98195, USA
Geraghty, D.E., and Olson, M.V.
Direct Submission
Submitted (08-DEC-1998) Human Genome Center

REMARK
Washington, Box 352145, Seattle, WA 98195, USA
University of Washington Human Genome Center
Box 352145 Seattle, WA 98195
Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
On Dec 8, 1998 this sequence version replaced gi:2905865.
Overlapping Sequences:

Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

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DS or two chemistry coverage: 77.6%
Single stranded regions: 100.0%
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Sequence Validation: 0
This sequence has been validated

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Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400–600bp are not mapped and hence do not appear in the table. There are significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

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2289.48	2257.00	3644.92	3560.00	9333.67	9154.00
5302.18	5207.00	5611.48	5525.00	814.06	801.00
894.03	880.00	4618.79	4525.00	10116.87	9863.00
3041.57	2999.00	1532.79	1530.00	2432.75	2413.00
14697.70	14691.00	1726.25	1724.00		

FEATURES
source

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Source
Location/Qualifiers
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